

SEQUENCE LISTING

<110> Zauderer, Maurice
Paris, Mark J.
Smith, Ernest S.

<120> Targeted MHC Class I Alpha3 Vaccine Delivery Systems

<130> 1843.0120001

<150> US 60/457,896
<151> 2003-03-28

<160> 53

<170> PatentIn version 3.2

<210> 1
<211> 276
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<213> Homo sapiens

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gaccagaccc aggacacgga gctcgtggag accaggcctg cagggatgg aacttccag 180
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<212> DNA
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<223> Assembled Ig Gamma Heavy Chain

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cttccccgaa ccggtgacgg tgcgtggaa ctcaggcgcc ctgaccagcg gctgcacac 240
cttccccggct gtcctacagt cctcaggact ctactccctc agcagcgtcg tgaccgtgcc 300
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caagggtggac aagaaagttg agcccaaattc ttgtgacaaa actcacacat gcccaccgtg 420
cccagcacct gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga 480
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caactacaag	accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	960
gctcaccgtg	gacaagagca	ggtggcagca	gggaaacgtc	ttctcatgct	ccgtgatgca	1020
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<220>
<223> Ig alpha3 assembled chimera

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ggagatcaca ctgacctggc agcgggatgg ggaggaccag acccaggaca cggagctcgt	1860
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<210> 4
<211> 659
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig alpha3 assembled chimera

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Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
210 215 220

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
225 230 235 240

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
245 250 255

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
260 265 270

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
275 280 285

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
290 295 300

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
305 310 315 320

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
325 330 335

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
340 345 350

Gly Lys Gly Gly Ser Ser Asp Ala Pro Lys Thr His Met Thr His
355 360 365

His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser
370 375 380

Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp
385 390 395 400

Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly
405 410 415

Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln
420 425 430

Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr
435 440 445

Leu Arg Trp Gly Gly Ser Ser Glu Phe Gly Gly Ser Ser Asp
450 455 460

Ala Pro Lys Thr His Met Thr His Ala Val Ser Asp His Glu Ala
465 470 475 480

Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu
485 490 495

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
500 505 510

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
515 520 525

Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His
530 535 540

Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Gly Gly Ser Ser
545 550 555 560

Arg Ser Gly Gly Ser Ser Asp Ala Pro Lys Thr His Met Thr His
565 570 575

His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser

580

585

590

Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp
595 600 605

Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly
610 615 620

Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln
625 630 635 640

Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr
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Leu Arg Trp

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gctcaggtgg gtcaggaggc atccagcgta ctccaaagat tcaggtttac tcacgtcattc 180
cagcagagaa tggaaagtca aatttcctga attgctatgt gtctgggttt catccatccg 240
acattgaagt tgacttactg aagaatggag agagaattga aaaagtggag cattcagact 300
tgtcttcag caaggactgg tctttctatc tcttgtacta cactgaattc acccccactg 360
aaaaagatga gtatgcctgc cgtgtgaacc atgtgacttt gtcacagccc aagatagtta 420
agtgggatcg agacatgtaa ggatcccg 448

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<220>
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20 25 30

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ile Gln Arg Thr
35 40 45

Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser
50 55 60

Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu
65 70 75 80

Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser
85 90 95

Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr
100 105 110

Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His
115 120 125

Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met
130 135 140

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Ser Val Ala Pro Pro Pro Glu Glu Val
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<210> 8
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Val Ala Pro Pro Pro Glu Glu Val
1 5

<210> 9
<211> 8
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<400> 9

Glu Val Glu Pro Gly Ser Gly Val

1 5

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<212> PRT
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Glu Val Glu Pro Gly Ser Gly Val Arg Ile
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<210> 11
<211> 8
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<210> 12
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<400> 12

Ala Thr Tyr Leu Glu Leu Ala Ser Ala
1 5

<210> 13
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<400> 13

Ala Thr Tyr Leu Glu Leu Ala Ser Ala Val
1 5 10

<210> 14
<211> 8
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Tyr Leu Glu Leu Ala Ser Ala Val
1 5

<210> 15
<211> 10
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<213> Homo sapiens

<400> 15

Ser Ala Val Lys Glu Gln Tyr Pro Gly Ile
1 5 10

<210> 16

<211> 9

<212> PRT

<213> Homo sapiens

<400> 16

Ala Val Lys Glu Gln Tyr Pro Gly Ile
1 5

<210> 17

<211> 8

<212> PRT

<213> Homo sapiens

<400> 17

Gly Ile Glu Ile Glu Ser Arg Leu
1 5

<210> 18

<211> 9

<212> PRT

<213> Homo sapiens

<400> 18

Glu Ile Glu Ser Arg Leu Gly Gly Thr
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<210> 19

<211> 10

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<400> 19

Arg Leu Gly Gly Thr Gly Ala Phe Glu Ile
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<211> 9

<212> PRT

<213> Homo sapiens

<400> 20

Gly Thr Gly Ala Phe Glu Ile Glu Ile
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<210> 21

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<400> 21

Glu Ile Glu Ile Asn Gly Gln Leu
1 5

<210> 22
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<212> PRT
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<400> 22

Glu Ile Glu Ile Asn Gly Gln Leu Val
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<210> 23
<211> 9
<212> PRT
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<400> 23

Asp Leu Ile Glu Ala Ile Arg Arg Ala
1 5

<210> 24
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Leu Ile Glu Ala Ile Arg Arg Ala
1 5

<210> 25
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<400> 25

Ala Ile Arg Arg Ala Ser Asn Gly Glu Thr
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<210> 26
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<400> 26

Arg Ala Ser Asn Gly Glu Thr Leu

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<210> 27
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1 5 10

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Ile Thr Asn Ser Arg Pro Pro Cys Val
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<400> 29

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<210> 30
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<210> 31
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Glu Pro Cys Gly Phe Glu Ala Thr Tyr
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<210> 32
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<400> 32

Ala Ser Asn Gly Glu Thr Leu Glu Lys
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<213> Unknown

<220>
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<210> 34
<211> 15
<212> PRT
<213> Unknown

<220>
<223> Synthetic peptide linker

<400> 34

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1 5 10 15

<210> 35
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<212> DNA
<213> Unknown

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<223> N may be any nucleotide

<220>
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<222> (10)..(10)
<223> May be repeated from 10 up to 20 times

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<220>
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<223> May be repeated from 10 up to 20 times

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<220>
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<400> 37
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<211> 28
<212> DNA
<213> Unknown

<220>
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28

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<223> Synthetic oligonucleotide PCR primers	
<400> 44	
gaagatctgg aggccgttct tcagacgccc ccaaaaacg	38
<210> 45	
<211> 38	
<212> DNA	
<213> Unknown	
<220>	
<223> Synthetic oligonucleotide PCR primers	
<400> 45	
aattgcggcc gcaaaccatg ggatggagct gtatcatc	38

<210> 46
<211> 33
<212> DNA
<213> Unknown

<220>
<223> Synthetic oligonucleotide PCR primers

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tgaagaacct cctccttac ccggagacag gga 33

<210> 47
<211> 83
<212> DNA
<213> Unknown

<220>
<223> Synthetic oligonucleotide

<400> 47
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tggaggctaa cctggtgccc atg 83

<210> 48
<211> 83
<212> DNA
<213> Unknown

<220>
<223> Synthetic oligonucleotide

<400> 48
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cacggagcga gacatatcga tgg 83

<210> 49
<211> 87
<212> DNA
<213> Unknown

<220>
<223> Synthetic oligonucleotide

<400> 49
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gggtcaggag gcatccagcg tactcca 87

<210> 50
<211> 87
<212> DNA
<213> Unknown

<220>
<223> Synthetic oligonucleotide

<400> 50
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aaccgttagcc accatgggca ccaggtt 87

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<211> 21
<212> DNA
<213> Unknown

<220>
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<400> 51
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<210> 52
<211> 29
<212> DNA
<213> Unknown

<220>
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<400> 52
cgggatcctt acatgtctcg atcccactt 29

<210> 53
<211> 10
<212> PRT
<213> Human immunodeficiency virus

<400> 53
Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
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